

R. Schwachner

1644

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/881,509

DATE: 04/22/1999  
TIME: 11:56:26

INPUT SET: S31576.raw

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: SCHENDEL, Dolores J.  
6  
7 (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA  
8  
9 (iii) NUMBER OF SEQUENCES: 44  
10  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP  
13 (B) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby  
14 (C) CITY: Washington  
15 (D) STATE: DC  
16 (E) COUNTRY: USA  
17 (F) ZIP: 20005-5701  
18  
19 (vi) CURRENT APPLICATION DATA:  
20 (A) APPLICATION NUMBER: 08/881,509  
21 (B) FILING DATE: June 24, 1997  
22 (C) CLASSIFICATION:  
23  
24 (viii) ATTORNEY/AGENT INFORMATION:  
25 (A) NAME: Kitts, Monica Chin  
26 (B) REGISTRATION NUMBER: 36,105  
27 (C) REFERENCE/DOCKET NUMBER: 564-7015  
28  
29 (ix) TELECOMMUNICATION INFORMATION:  
30 (A) TELEPHONE: (202) 638-5000  
31 (B) TELEFAX: (202) 638-4810  
32

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE

add these  
MANDATORY headings  
and responses for a  
U.S. case

ERRORED SEQUENCES FOLLOW:

204 (2) INFORMATION FOR SEQ ID NO: 3:  
205  
206 (i) SEQUENCE CHARACTERISTICS:  
--> 207 (A) LENGTH: 936 base pairs  
208 (B) TYPE: nucleic acid  
209 (C) STRANDEDNESS: both  
210 (D) TOPOLOGY: linear

(next page)

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/881,509DATE: 04/22/1999  
TIME: 11:56:26

INPUT SET: S31576.raw

211  
212 (ix) FEATURE:  
213 (A) NAME/KEY: CDS  
214 (B) LOCATION:1..933  
215  
216 (ix) FEATURE:  
217 (A) NAME/KEY: sig\_peptide  
218 (B) LOCATION:1..63  
219  
220 (ix) FEATURE:  
221 (A) NAME/KEY: mat\_peptide  
222 (B) LOCATION:64..933  
223  
224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
225  
226 ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA 48  
227 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala  
228 -21 -20 -15 -10  
229  
230 GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA 96  
231 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr  
232 -5 1 5 10  
233  
234 CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC 144  
235 Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His  
236 15 20 25  
237  
238 TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT 192  
239 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe  
240 30 35 40  
241  
242 CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC 240  
243 Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe  
244 45 50 55  
245  
246 GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG  
247 288  
248 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu  
249 60 65 70 75  
250  
--> 251 AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC 336 OK  
252 Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala  
253 80 85 90  
254  
255 AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG 384  
256 Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg  
257 95 100 105  
258  
259 CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT 432  
260 Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala  
261 110 115 120  
262  
263 GTG TTT GAG CCA TCA GAA GCA GAG ATC TCC CAC ACC CAA AAG GCC ACA 480

288  
mud up

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/881,509DATE: 04/22/1999  
TIME: 11:56:26

INPUT SET: S31576.raw

264	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	
265		125					130					135					
266																	
267	CTG	GTG	TGC	CTG	GCC	ACA	GGC	TTC	TAC	CCC	GAC	CAC	GTG	GAG	CTG	AGC	528
268	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	
269	140					145				150					155		
270																	
271	TGG	TGG	GTG	AAT	GGG	AAG	GAG	GTG	CAC	AGT	GGG	GTC	AGC	ACA	GAC	CCG	576
272	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	
273					160					165					170		

please ignore  
blank section

08/881,509

274																			
275	CAG	CCC	CTC	AAG	GAG	CAG	CCC	GCC	CTC	AAT	GAC	TCC	AGA	TAC	TGC	CTG			624
276	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu			
277				175					180						185				
278																			
279	AGC	AGC	CGC	CTG	AGG	GTC	TCG	GCC	ACC	TTC	TGG	CAG	AAC	CCC	CGC	AAC			672
280	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn			
281			190					195					200						
282																			
283	CAC	TTC	CGC	TGT	CAA	GTC	CAG	TTC	TAC	GGG	CTC	TCG	GAG	AAT	GAC	GAG			720
284	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu			
285		205					210					215							
286																			
287	TGG	ACC	CAG	GAT	AGG	GCC	AAA	CCT	GTC	ACC	CAG	ATC	GTC	AGC	GCC	GAG			768
288	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu			
289	220					225					230					235			
290																			
291	GCC	TGG	GGT	AGA	GCA	GAC	TGT	GGC	TTC	ACC	TCC	GAG	TCT	TAC	CAG	CAA			816
292	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln			
293				240						245					250				
294																			
295	GGG	GTC	CTG	TCT	GCC	ACC	ATC	CTC	TAT	GAG	ATC	TTG	CTA	GGG	AAG	GCC			864
296	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala			
297			255					260						265					
298																			
299	ACC	TTG	TAT	GCC	GTG	CTG	GTC	AGT	GCC	CTC	GTG	CTG	ATG	GCC	ATG	GTC			912
300	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val			
301			270					275					280						
302																			
303	AAG	AGA	AAG	GAT	TCC	AGA	GGC	TAG											936
304	Lys	Arg	Lys	Asp	Ser	Arg	Gly												
305		285					290												
306																			
307																			

654 (2) INFORMATION FOR SEQ ID NO: 22:

655

656 (i) SEQUENCE CHARACTERISTICS:

--> 657 (A) LENGTH: 20 base pairs

658 (B) TYPE: nucleic acid

659 (C) STRANDEDNESS: single

660 (D) TOPOLOGY: linear

661

next page

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/881,509

DATE: 04/22/1999  
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INPUT SET: S31576.raw

662 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

663

664 TAGAGGATGG TGGCAGACAG

665

666

206 insert  
cumulative  
base total  
at right  
margin

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/881,509**DATE: 04/22/1999  
TIME: 11:56:27*INPUT SET: S31576.raw*

Line	Error	Original Text
207	Entered (936) and Calc. Seq. Length (888) differ	(A) LENGTH: 936 base pairs
251	# of Sequences for line conflicts w/ running total	AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GC
657	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 base pairs

PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/08/881,509**

DATE: 04/22/1999  
TIME: 11:56:27

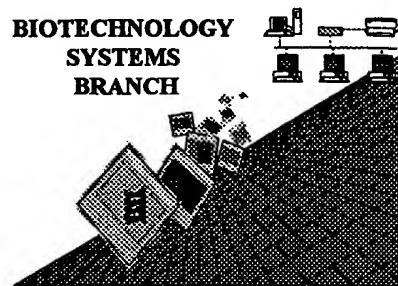
*INPUT SET: S31576.raw*

MEDIUM TYPE  
COMPUTER  
OPERATING SYSTEM  
SOFTWARE  
COMPUTER READABLE FORM  
APPLICATION NUMBER  
FILING DATE  
PRIOR APPLICATION DATA

Schwadron

# **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/881,509

Art Unit / Team No. :

1644

Date Processed by STIC:

4/22/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

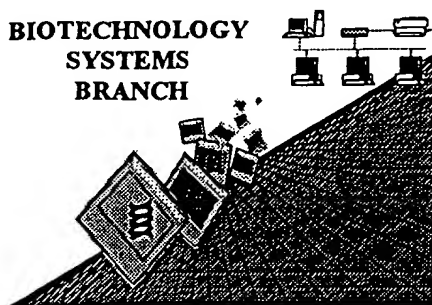
**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**





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### Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>  
The software is in current directory: `pub/checker/`  
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441  
WASHINGTON DC 20231

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*For Further Information, Contact: **Arti Shah at 703-308-4212***

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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